



SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana  
White, David  
MacBeth, Kyle J.

<120> 2786, A NOVEL HUMAN AMINOPEPTIDASE

<130> MPI99-193CN2M

<140> US 10/767,308  
<141> 2004-01-29

<150> US 09/443,795  
<151> 1999-11-19

<150> US 10/056,253  
<151> 2002-01-24

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1  
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<212> PRT  
<213> Homo sapiens

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Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg  
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Ala Phe Glu Leu Leu His Leu Asp Leu Arg Ala Glu Phe Gly  
35 40 45  
Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val  
50 55 60  
Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu  
65 70 75 80  
Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Ala Leu Arg Arg Glu  
85 90 95  
Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr  
100 105 110  
Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln  
115 120 125  
Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Leu Thr Tyr Arg Val  
130 135 140  
Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly  
145 150 155 160  
Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg  
165 170 175  
Ala Phe Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser  
180 185 190  
Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser  
195 200 205  
Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Phe Gln Met Cys Gln  
210 215 220  
Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser  
225 230 235 240  
Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile  
245 250 255

Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala  
 260 265 270  
 Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu  
 275 280 285  
 Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys  
 290 295 300  
 Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala  
 305 310 315 320  
 Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val  
 325 330 335  
 Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met  
 340 345 350  
 Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr  
 355 360 365  
 Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp  
 370 375 380  
 Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu  
 385 390 395 400  
 Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys  
 405 410 415  
 Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp  
 420 425 430  
 Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg  
 435 440 445  
 Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro  
 450 455 460  
 Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp  
 465 470 475 480  
 Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser  
 485 490 495  
 Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp  
 500 505 510  
 Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser  
 515 520 525  
 Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln  
 530 535 540  
 Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr  
 545 550 555 560  
 Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly  
 565 570 575  
 Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys  
 580 585 590  
 Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr  
 595 600 605  
 His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu  
 610 615 620  
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 625 630 635 640  
 Val Gln Gln Ile Val Ala Pro Lys Gly Ser  
 645 650

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 <212> DNA  
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 <222> (62)...(2011)

<221> misc\_feature

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Met Ala Ser Gly Glu His Ser Pro Gly Ser Gly Ala Ala Arg Arg Pro			
1 5 10 15			
ctg cac tcc gcg cag gct gtg gac gtg gcc tcg gcc tcc aac ttc cgg	157		
Leu His Ser Ala Gln Ala Val Asp Val Ala Ser Ala Ser Asn Phe Arg			
20 25 30			
gcc ttt gag ctg ctg cac ttg cac ctg gac ctg cgg gct gag ttc ggg	205		
Ala Phe Glu Leu Leu His Leu His Leu Asp Leu Arg Ala Glu Phe Gly			
35 40 45			
cct cca ggg ccc ggc gca ggg agc cgg ggg ctg agc ggc acc gcg gtc	253		
Pro Pro Gly Pro Gly Ala Gly Ser Arg Gly Leu Ser Gly Thr Ala Val			
50 55 60			
ctg gac ctg cgc tgc ctg gag ccc gag ggc gcc gag ctg cgg ctg	301		
Leu Asp Leu Arg Cys Leu Glu Pro Glu Gly Ala Ala Glu Leu Arg Leu			
65 70 75 80			
gac tcg cac ccg tgc ctg gag gtg acg gcg gcg ctg cgg cgg gag	349		
Asp Ser His Pro Cys Leu Glu Val Thr Ala Ala Leu Arg Arg Glu			
85 90 95			
cgg ccc ggc tcg gag gag ccg cct gcg gag ccc gtg agc ttc tac acg	397		
Arg Pro Gly Ser Glu Glu Pro Pro Ala Glu Pro Val Ser Phe Tyr Thr			
100 105 110			
cag ccc ttc tcg cac tat ggc cag gcc ctg tgc gtg tcc ttc ccg cag	445		
Gln Pro Phe Ser His Tyr Gly Gln Ala Leu Cys Val Ser Phe Pro Gln			
115 120 125			
ccc tgc cgc gcc gag cgc ctc cag gtg ctg ctc acc tac cgc gtc	493		
Pro Cys Arg Ala Ala Glu Arg Leu Gln Val Leu Thr Tyr Arg Val			
130 135 140			
ggg gag gga ccc ggg gtt tgc tgg ttg gct ccc gag cag aca gca gga	541		
Gly Glu Gly Pro Gly Val Cys Trp Leu Ala Pro Glu Gln Thr Ala Gly			
145 150 155 160			
aag aag aag ccc ttc gtg tac acc cag ggc cag gct gtc cta aac cgg	589		
Lys Lys Lys Pro Phe Val Tyr Thr Gln Gly Gln Ala Val Leu Asn Arg			
165 170 175			
gcc ttc ttc cct tgc ttc gac acg cct gct gtt aaa tac aag tat tca	637		
Ala Phe Pro Cys Phe Asp Thr Pro Ala Val Lys Tyr Lys Tyr Ser			
180 185 190			
gct ctt att gag gtc cca gat ggc ttc aca gct gtg atg agt gct agc	685		
Ala Leu Ile Glu Val Pro Asp Gly Phe Thr Ala Val Met Ser Ala Ser			
195 200 205			
acc tgg gag aag aga ggt cca aat aag ttc ttc cag atg tgt cag	733		
Thr Trp Glu Lys Arg Gly Pro Asn Lys Phe Phe Gln Met Cys Gln			
210 215 220			
ccc atc ccc tcc tat ctg ata gct ttg gcc atc gga gat ctg gtt tcg	781		

Pro Ile Pro Ser Tyr Leu Ile Ala Leu Ala Ile Gly Asp Leu Val Ser			
225	230	235	240
gct gaa gtt gga ccc agg agc cgg gtg tgg gct gag ccc tgc ctg att			829
Ala Glu Val Gly Pro Arg Ser Arg Val Trp Ala Glu Pro Cys Leu Ile			
245	250	255	
gat gct gcc aat gag gag tac aac ggg gtg ata gaa gaa ttt ttg gca			877
Asp Ala Ala Asn Glu Glu Tyr Asn Gly Val Ile Glu Glu Phe Leu Ala			
260	265	270	
aca gga gag aag ctt ttt gga cct tat gtt tgg gga agg tat gac ttg			925
Thr Gly Glu Lys Leu Phe Gly Pro Tyr Val Trp Gly Arg Tyr Asp Leu			
275	280	285	
ctc ttc atg cca ccg tcc ttt cca ttt gga gga atg gag aac cct tgt			973
Leu Phe Met Pro Pro Ser Phe Pro Phe Gly Gly Met Glu Asn Pro Cys			
290	295	300	
ctg acc ttt gtc acc ccc tgc ctg cta gct ggg gac cgc tcc ttg gca			1021
Leu Thr Phe Val Thr Pro Cys Leu Leu Ala Gly Asp Arg Ser Leu Ala			
305	310	315	320
gat gtc atc atc cat gag atc tcc cac agt tgg ttt ggg aac ctg gtc			1069
Asp Val Ile Ile His Glu Ile Ser His Ser Trp Phe Gly Asn Leu Val			
325	330	335	
acc aac gcc aac tgg ggt gaa ttc tgg ctc aat gaa ggt ttc acc atg			1117
Thr Asn Ala Asn Trp Gly Glu Phe Trp Leu Asn Glu Gly Phe Thr Met			
340	345	350	
tac gcc cag agg agg atc tcc acc atc ctc ttt ggc gct gcg tac acc			1165
Tyr Ala Gln Arg Arg Ile Ser Thr Ile Leu Phe Gly Ala Ala Tyr Thr			
355	360	365	
tgc ttg gag gct gca acg ggg cgg gct ctg ctg cgt caa cac atg gac			1213
Cys Leu Glu Ala Ala Thr Gly Arg Ala Leu Leu Arg Gln His Met Asp			
370	375	380	
atc act gga gag gaa aac cca ctc aac aag ctc cgc gtg aag att gaa			1261
Ile Thr Gly Glu Glu Asn Pro Leu Asn Lys Leu Arg Val Lys Ile Glu			
385	390	395	400
cca ggc gtt gac ccg gac acc tat aat gag acc ccc tac gag aaa			1309
Pro Gly Val Asp Pro Asp Asp Thr Tyr Asn Glu Thr Pro Tyr Glu Lys			
405	410	415	
ggt ttc tgc ttt gtc tca tac ctg gcc cac ttg gtg ggt gat cag gat			1357
Gly Phe Cys Phe Val Ser Tyr Leu Ala His Leu Val Gly Asp Gln Asp			
420	425	430	
cag ttt gac agt ttt ctc aag gcc tat gtg cat gaa ttc aaa ttc cga			1405
Gln Phe Asp Ser Phe Leu Lys Ala Tyr Val His Glu Phe Lys Phe Arg			
435	440	445	
agc atc tta gcc gat gac ttt ctg gac ttc tac ttg gaa tat ttc cct			1453
Ser Ile Leu Ala Asp Asp Phe Leu Asp Phe Tyr Leu Glu Tyr Phe Pro			
450	455	460	
gag ctt aag aaa aag aga gtg gat atc att cca ggt ttt gag ttt gat			1501
Glu Leu Lys Lys Lys Arg Val Asp Ile Ile Pro Gly Phe Glu Phe Asp			
465	470	475	480

cga tgg ctg aat acc ccc ggc tgg ccc ccg tac ctc cct gat ctc tcc Arg Trp Leu Asn Thr Pro Gly Trp Pro Pro Tyr Leu Pro Asp Leu Ser 485 490 495	1549
cct ggg gac tca ctc atg aag cct gct gaa gag cta gcc caa ctg tgg Pro Gly Asp Ser Leu Met Lys Pro Ala Glu Glu Leu Ala Gln Leu Trp 500 505 510	1597
gca gcc gag gag ctg gac atg aag gcc att gaa gcc gtg gcc atc tct Ala Ala Glu Glu Leu Asp Met Lys Ala Ile Glu Ala Val Ala Ile Ser 515 520 525	1645
ccc tgg aag acc tac cag ctg gtc tac ttc ctg gat aag atc ctc cag Pro Trp Lys Thr Tyr Gln Leu Val Tyr Phe Leu Asp Lys Ile Leu Gln 530 535 540	1693
aaa tcc cct ctc cct ggg aat gtg aaa aaa ctt gga gac aca tac Lys Ser Pro Leu Pro Pro Gly Asn Val Lys Lys Leu Gly Asp Thr Tyr 545 550 555 560	1741
cca agt atc tca aat gcc cgg aat gca gag ctc cgg ctg cga tgg ggc Pro Ser Ile Ser Asn Ala Arg Asn Ala Glu Leu Arg Leu Arg Trp Gly 565 570 575	1789
caa atc gtc ctt aag aac gac cac cag gaa gat ttc tgg aaa gtg aag Gln Ile Val Leu Lys Asn Asp His Gln Glu Asp Phe Trp Lys Val Lys 580 585 590	1837
gag ttc ctg cat aac cag ggg aag cag aag tat aca ctt ccg ctg tac Glu Phe Leu His Asn Gln Gly Lys Gln Lys Tyr Thr Leu Pro Leu Tyr 595 600 605	1885
cac gca atg atg ggt ggc agt gag gtg gcc cag acc ctc gcc aag gag His Ala Met Met Gly Gly Ser Glu Val Ala Gln Thr Leu Ala Lys Glu 610 615 620	1933
act ttt gca tcc acc gcc tcc cag ctc cac agc aat gtt gtc aac tat Thr Phe Ala Ser Thr Ala Ser Gln Leu His Ser Asn Val Val Asn Tyr 625 630 635 640	1981
gtc cag cag atc gtg gca ccc aag ggc agt tagaggctcg tgtgcattggc Val Gln Gln Ile Val Ala Pro Lys Gly Ser 645 650	2031
ccctgcctct tcaggctctc caggcttca gaataattgt ttgttccaa attcctgttc cctgatcaac ttccctggagt ttatatcccc tcaggataat ctattctcta gcttaggtat ctgtgactct tggccctctg ctctgggg aacttacttc tctatagccc actgagcccc gagacagaga acctgcccac agctctcccc gctacaggct gcaggcactg cagggcagcg ggtattctcc tccccaccta agtctctggg aagaagtgg aaggactgat gctcttcttt tttctcttc tgtcctttt cttgctgatt ttatgcaaaag ggctggcatt ctgattgttc tttttcagg ttaatcctt attttaataa agtttcaag caaaaattaa aaaaaaaaaa aaaaaaaaa	2091 2151 2211 2271 2331 2391 2451 2459
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<223> Ribonucleoprotein Binding Site	

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1 5 10 15
Gly Ser Cys Ile Phe Tyr Leu Ile Val Ala Xaa Phe Tyr Met
20 25 30

<210> 4
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Nuclear Localization Motif

<400> 4
Lys Lys Lys
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<210> 5
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Ribnucleoprotein Binding Motif

<400> 5
Lys Gly Tyr Cys Phe Val Ser Tyr
1 5

<210> 6
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> potential catalytic site

<400> 6
His Glu Ile Ser His
1 5

<210> 7
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> potential catalytic site

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Trp Leu Asn Glu
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<210> 8  
<211> 24  
<212> PRT  
<213> Artificial Sequence

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<223> Zinc Binding Consensus Sequence

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<221> VARIANT  
<222> (6)...(23)  
<223> Xaa = any amino acid

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Xaa Xaa Xaa Xaa Xaa Xaa Glu  
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